

RESULT 3 for SEQ ID NO: 453

AW006758
 LOCUS AW006758 362 bp mRNA linear EST 08-MAR-2000
 DEFINITION wt07a10.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2506746 3',
 mRNA sequence.
 ACCESSION AW006758
 VERSION AW006758.1 GI:5855536
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 362)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Tumor Gene Index
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.
 , Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arraying: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 442 Std Error: 0.00
 Seq primer: -40UP from Gibco.

FEATURES Location/Qualifiers
 source 1..362
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2506746"
 /clone_lib="NCI_CGAP_Co3"
 /sex="pooled"
 /tissue_type="colon"
 /lab_host="DH10B"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from 12 pooled bulk tumor samples and primed
 with a Not I - oligo(dT) primer. Double-stranded cDNA was
 ligated to Eco RI adaptors (Pharmacia), digested with Not
 I and cloned into the Not I and Eco RI sites of the
 modified pT7T3 vector. Library went through one round of
 normalization."

BASE COUNT 82 a 93 c 91 g 96 t
 ORIGIN

Query Match 100.0%; Score 330; DB 10; Length 362;
 Best Local Similarity 100.0%; Pred. No. 6.3e-89;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTGGATAAATATATTAGCAAATAAATATTTCTAACATAGTGCCTGATTCAAGCGTC 60
 Db 1 TGTGGATAAATATATTAGCAAATAAATATTTCTAACATAGTGCCTGATTCAAGCGTC 60
 Qy 61 TGTCTGGTTACAGATATAATACCCATGTGGGTACCTAGGTGCTAGTCTCCCCACTAAC 120
 Db 61 TGTCTGGTTACAGATATAATACCCATGTGGGTACCTAGGTGCTAGTCTCCCCACTAAC 120
 Qy 121 AGGGAAAAAGGTTCCCAAGGTGGGTCTCTGCCACCTTGCACCACATTACACATTCAA 180
 Db 121 AGGGAAAAAGGTTCCCAAGGTGGGTCTCTGCCACCTTGCACCACATTACACATTCAA 180
 Qy 181 ATGGGATAATGCCCTGAGGGCCAAGAGTGTCAGGCTGCCCTGGGTGAATGTCACCC 240
 Db 181 ATGGGATAATGCCCTGAGGGCCAAGAGTGTCAGGCTGCCCTGGGTGAATGTCACCC 240
 Qy 241 ATGAGGCCCATCAGCTCTGTCCACTCAGTGAGGCCAGACTGTGCTTAATCCACTCTC 300
 Db 241 ATGAGGCCCATCAGCTCTGTCCACTCAGTGAGGCCAGACTGTGCTTAATCCACTCTC 300
 Qy 301 CTGTGGGTCCCTGGCCTGTATGGCTTATAC 330
 Db 301 CTGTGGGTCCCTGGCCTGTATGGCTTATAC 330

RESULT 4
ABV29346
ID ABV29346 standard; cDNA; 734 BP.
XX
AC ABV29346;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 29337.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX
PS Claim 1; Page 6285; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 734 BP; 193 A; 157 C; 114 G; 218 T; 52 other;

Query Match 100.0%; Score 320; DB 23; Length 734;
Best Local Similarity 100.0%; Pred. No. 1.1e-82;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CACAGTGGCAGATTTCTTAATAGATATAATTCAAACAGATACAACAAATTAAAAATC	60
Db	93	CACAGTGGCAGATTTCTTAATAGATATAATTCAAACAGATACAACAAATTAAAAATC	152
Qy	61	TAATTCAACGGCAGGTAAACATGGGTGCTCAAAAAGTCCACATAGACATTACACTTGGG	120
Db	153	TAATTCAACGGCAGGTAAACATGGGTGCTCAAAAAGTCCACATAGACATTACACTTGGG	212
Qy	121	CCATCAGTATTCCCTCACATCCCTTTGTTAAGTCCCATTTCGCAGTGGCAGTACAG	180
Db	213	CCATCAGTATTCCCTCACATCCCTTTGTTAAGTCCCATTTCGCAGTGGCAGTACAG	272
Qy	181	GAGAAATCTCCACCCCTCACCGCACAATCCACCGCGCATTACCACTGAAGTGAAGGTC	240
Db	273	GAGAAATCTCCACCGTCACCGCACAATCCACCGCGCATTACCACTGAAGTGAAGGTC	332
Qy	241	TCATCTCGAAGGTGCGCTCAGCCATAAAAGAAAACATATTACAGAAAGGAAAATAAGT	300
Db	333	TCATCTCGAAGGTGCGCTCAGCCATAAAAGAAAACATATTACAGAAAGGAAAATAAGT	392
Qy	301	GTGCTCTTCCCACCCGCAA 320	
Db	393	GTGCTCTTCCCACCCGCAA 412	

RESULT 4
AI368176
LOCUS AI368176 392 bp mRNA linear EST 13-FEB-1999
DEFINITION qk65b10.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1873819 3',
 mRNA sequence.
ACCESSION AI368176
VERSION AI368176.1 GI:4137921
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 392)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/Image.html
 Insert Length: 1195 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 381.

FEATURES Location/Qualifiers
source 1..392
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1873819"
 /clone_lib="NCI_CGAP_Co8"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B"
 /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 121 a 102 c 65 g 104 t
ORIGIN

 Query Match 100.0%; Score 320; DB 9; Length 392;
 Best Local Similarity 100.0%; Pred. No. 8.6e-66;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 CACAGTGGCAGATTTCTTAATAGATATATTCAACAGATA
 CACAACAAATTAAAAAATC 60
 |||||
 Db 6 CACAGTGGCAGATTTCTTAATAGATATATTCAACAGATA
 CACAACAAATTAAAAAATC 65

 Qy 61 TAATTCACGGCAGGTAAACATGGGTGCTCAAAAGTT
 CACATAGACATTACACTTGGG 120
 |||||
 Db 66 TAATTCACGGCAGGTAAACATGGGTGCTCAAAAGTT
 CACATAGACATTACACTTGGG 125

 Qy 121 CCATCAGTATTCCCTCACATTCCCTTGT
 TAAGTCCCACATTCGCAGTGGCAGTACAG 180
 |||||
 Db 126 CCATCAGTATTCCCTCACATTCCCTTGT
 TAAGTCCCACATTCGCAGTGGCAGTACAG 185

 Qy 181 GAGAAATCTCCACCGTCA
 CCGACAATCCACCAGGCGCATTAC 240
 |||||
 Db 186 GAGAAATCTCCACCGTCA
 CCGACAATCCACCAGGCGCATTAC 245

 Qy 241 TCATCTCGAAGGTGCGTCAGCCATA
 AAAAGAAAAACATATTACAGAAGGAAAAATAAGT 300
 |||||
 Db 246 TCATCTCGAAGGTGCGTCAGCCATA
 AAAAGAAAAACATATTACAGAAGGAAAAATAAGT 305

 Qy 301 GTGCTCTTCCCACCGCAA 320
 |||||
 Db 306 GTGCTCTTCCCACCGCAA 325

RESULT 2
 AA629913
 LOCUS AA629913 467 bp mRNA linear EST 06-MAR-1998
 DEFINITION ad45e02.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone
 IMAGE:884666 3' similar to contains Alu repetitive element; contains
 element MER22 repetitive element ;, mRNA sequence.
 ACCESSION AA629913
 VERSION AAG29913.1 GI:2552524
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 467)
 AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
 Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
 ,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
 White,Y., Wylie,T., Waterston,R. and Wilson,R.
 TITLE WashU-NCI human EST Project
 JOURNAL Unpublished (1997)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 742 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham.
 FEATURES Location/Qualifiers
 source 1..467
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:884666"
 /clone_lib="Stratagene lung carcinoma 937218"
 /tissue_type="lung carcinoma"
 /cell_line="NCI-H69"
 /dev_stage="cell line NCI-H69"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI
 ; Site_2: XbaI; Cloned unidirectionally. Primer: Oligo
 dT. Small cell carcinoma cell line NCI-H69. Average
 insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
 sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
 CTCGAGTTTTTTTTTTTTTTTT 3'"
 BASE COUNT 98 a 110 c 114 g 145 t
 ORIGIN

Query Match 96.5%; Score 453.6; DB 9; Length 467;
 Best Local Similarity 98.9%; Pred. No. 5.3e-86;
 Matches 456; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	10	GGAGGTTTATTATTTTATTATTTGAGACTGAGTCTTGTCTGTCACTCAGGCTGGA 69
Db	7	GGAGGTTTATTATTTTATTATTTGAGACTGAGTCTTGTCTGTCACTCAGGCTGGA 66
Qy	70	GTGCAGTGGCTCACTGCAACCTCCGCCTCCAGGTTCAAGCAATTCTCTGCCTCAGCCT 129
Db	67	GTGCAGTGGCTCACTGCAACCTCCGCCTCCAGGTTCAAGCAATTCTCTGCCTCAGCCT 126
Qy	130	CCCTAGTAGCTGGGATTACAGGTGTCCACCCATGCCCAATTAAATTTGTATTTGG 189
Db	127	CCCTAGTAGCTGGGATTACAGGTGTCCACCCATGCCCAATTAAATTTGTATTTGG 186
Qy	190	TACAGACAGGGTTTACCCATGTTGGCCAGGATGGTCTCGATCTGTTGACCTTGATCC 249
Db	187	TACAGACAGGGTTTACCCATGTTGGCCAGGATGGTCTCGATCTGTTGACCTTGATCC 246
Qy	250	GCCTGCCTCGGCCTCCAAAGTGGCTGGGATTACAGGCGTCAACCCNGCCCTGGACTACT 309
Db	247	GCCTGCCTCGGCCTCCAAAGTGGCTGGGATTACAGGCGTCAACCCNGCCCTGGACTACT 306
Qy	310	TATGGAGGTTTAAAAATCTTTAAGTCCAGGCCCTGACGTTAGAGAAGGTTACAAAGG 369
Db	307	TATGGAGGTTTAAAAATCTTTAAGTCCAGGCCCTGACGTTAGAGAAGGTTACAAAGG 366
Qy	370	CGGCCAGGATCTGAGTATTCCAAAAAGCTGGGAGGCAGCTGAGGTTCCCTCCAGT 429
Db	367	CGGCCAGGATCTGAGTATTCCAAAAAGCTGGGAGGCAGCTGAGGTTCCCTCCAGT 426
Qy	430	TGAATCACTGACTTGTAGGTCGACTGGGGTACTTTGGGTTT 470
Db	427	TGAATCACTGACTTGTAGGTCGACTGGGGTACTTTGGGTTT 467

BASE COUNT	597	a	428	c	397	g	549	t			
ORIGIN											
Query	Match	100.0%	Score	1971	DB	9	Length	1971			
Best local	Similarity	100.0%	Pred. No.	0	Mismatches	0	Indels	0			
Matches	1971	Conservative	0	0	0	0	Gaps	0			
Qy	1	GTCATGGGTCATCCCAACTCTGGCGCTGGAAACCTGGCTTCCTCGCTCAGCTG	60	Qy	1	GIGATGGCTCATCCCAACATGGCGCTGGAAACCTGGCTTCCTCGCTCAGCTG	60	Qy	1	ATACTCCCTACTATGGACCCGACATGGACTTTAGAACCTGGAACTGGAACTCCA	120
Db	61	ATACTCCCTACTATGGACCCGACATGGACTTTAGAACCTGGAACTGGAACTCCA	120	Db	61	ATACTCCCTACTATGGACCCGACATGGACTTTAGAACCTGGAACTGGAACTCCA	120	Db	121	GGGCCACACCTGCGCTTGGGAATGCTTGCTGCTGGCTTGGAACTGGAACTCCA	180
Qy	121	GGGCCACACCTGCGCTTGGGAATGCTTGCTGCTGGCTTGGAACTGGAACTCCA	180	Db	121	GGGCCACACCTGCGCTTGGGAATGCTTGCTGCTGGCTTGGAACTGGAACTCCA	180	Db	121	GGGCCACACCTGCGCTTGGGAATGCTTGCTGCTGGCTTGGAACTGGAACTCCA	180
Qy	181	TTTGGACATGGAAAGTTATAAAGATGATAAAGTGAAGTGTGAAAGTGTGAACTGACAG	240	Qy	181	TTTGGACATGGAAAGTTATAAAGATGATAAAGTGAAGTGTGAAAGTGTGAACTGACAG	240	Qy	241	CCTATGGGGCTACAGATCCGACTGTCAGTCAAACAGTGTGCTGAAAGTGTGAACTGACAG	300
Db	241	CCTATGGGGCTACAGATCCGACTGTCAGTCAAACAGTGTGCTGAAAGTGTGAACTGACAG	300	Db	241	CCTATGGGGCTACAGATCCGACTGTCAGTCAAACAGTGTGCTGAAAGTGTGAACTGACAG	300	Qy	301	TCTGCTTCAACACGGAGGCTTCCGGCCAGTGGATTATGAAATGCCATCT	360
Qy	301	TCTGCTTCAACACGGAGGCTTCCGGCCAGTGGATTATGAAATGCCATCT	360	Db	301	TCTGCTTCAACACGGAGGCTTCCGGCCAGTGGATTATGAAATGCCATCT	360	Db	361	ATAGCTGGAGATGAGAAGATGGAGAGAATAGCTGAGATGAGATGAGATGTT	420
Db	361	ATAGCTGGAGATGAGAAGATGGAGAGAATAGCTGAGATGAGATGAGATGTT	420	Qy	421	GGAAACCTCAAGGAGATGTCCTATCTGTGCCAGTTGGAGATGAGATGTT	480	Qy	421	GGAAACCTCAAGGAGATGTCCTATCTGTGCCAGTTGGAGATGAGATGTT	480
Qy	421	GGAAACCTCAAGGAGATGTCCTATCTGTGCCAGTTGGAGATGAGATGTT	480	Db	421	GGAAACCTCAAGGAGATGTCCTATCTGTGCCAGTTGGAGATGAGATGTT	480	Db	481	CTGGGGGAAACGAGACAGGACAGGACAGCTGACCTTGAAACACGCTTGGGCCAC	540
Qy	481	CTGGGGGAAACGAGACAGGACAGGACAGCTGACCTTGAAACACGCTTGGGCCAC	540	Db	481	CTGGGGGAAACGAGACAGGACAGGACAGCTGACCTTGAAACACGCTTGGGCCAC	540	Db	541	AGCATGGTGTACATCATGTTGGAGATGAGATGTTGGAGAAT	600
Qy	541	AGCATGGTGTACATCATGTTGGAGATGAGATGTTGGAGAAT	600	Db	541	AGCATGGTGTACATCATGTTGGAGATGAGATGTTGGAGAAT	600	Db	601	CAAGACCCCTTGGAACACCAACACCAAGACGCTTAACTTACATCCATAGCCATTC	660
Qy	601	CAAGACCCCTTGGAACACCAACACCAAGACGCTTAACTTACATCCATAGCCATTC	660	Db	601	CAAGACCCCTTGGAACACCAACACCAAGACGCTTAACTTACATCCATAGCCATTC	660	Qy	661	GTCTCTTAAAGTTTCATCTTACCCAACTCTTGAACTTAAATCT	720
Qy	661	GTCTCTTAAAGTTTCATCTTACCCAACTCTTGAACTTAAATCT	720	Db	661	GTCTCTTAAAGTTTCATCTTACCCAACTCTTGAACTTAAATCT	720	Qy	721	GTGTTCTTAAAGTTTCATCTTACCCAACTCTTGAACTTAAATCT	780
Qy	721	GTGTTCTTAAAGTTTCATCTTACCCAACTCTTGAACTTAAATCT	780	Db	721	GTGTTCTTAAAGTTTCATCTTACCCAACTCTTGAACTTAAATCT	780	Qy	781	CGCTCAAGAGACAGACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	840
Db	781	CGCTCAAGAGACAGACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	840	Qy	841	AATCAAAAGACTCTGACACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900	Db	841	AATCAAAAGACTCTGACACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900
Qy	901	AATCAAAAGACTCTGACACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900	Db	901	AATCAAAAGACTCTGACACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900	Qy	961	GAATGGGCACTACCCGATGTCAGAGAAAGTCAGAAGGAATTGATACAGTTA	1020

HOMYPPFLA
HOMYPPFLA
Homo sapiens mRNA for cytochrome P-450 HFLa, complete cds.
D00408
D00408.1
GI:220148
CYP3A6; cytochrome P-450; human fetal liver cytochrome P-450.
Homo sapiens fetus liver cDNA to mRNA.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
I (bases 1 to 1971)
Komori, M., Nishio, K., Ohi, H., Kitada, M. and Kanataki, T.
Molecular cloning and sequence analysis of cDNA containing the entire coding region for human fetal liver cytochrome P-450. J. Biochem. 105 (2), 161-163 (1989)
8025154
COMMENT
Submitted in computer readable form by M. Komori on 15-Apr-1989. The deduced N-terminal amino acid sequence was identical to that of P-450 HFLa.
FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="liver"
/dev_stage="fetus"
/note="106 bp upstream of HindIII site. -clones
lambda-HFL33, lambda -HFL10"
CDS
4. .1515
/codon_start=1
/product="cytochrome P-450 HFLa"
/protein_id="BA00310.1"
/db_xref="GI:220149"
/translation="MOLIPNHLAVETWLLAIVSLLVLYKTRPHGLEKKLGIPGPPLPFLQNLSPFKRQKRVVYKQKRLVQKLSLSPFSLRKLKEVPTAOGYGVLRFLRELETGPKTFLHVEGASMDVTSFSGVSDSLNNEQDPVVENTKLRNLPDPFVSKVPPFLPFLDEALNTTVERKVISPLTSVSKVQKREGRKETOKHVRPQMLIDSONSKDSETHKALSLMAOSITIFVAGYETSSVLSFELVLEAHPPWDQKOMIDWLPNKEAPTDWQMLILOVNEFLRIPVAMKLRVCKDUEFNGMIPGVVMPISVILHDPWTEPEKFLPERFSRKNKONIDPYTTPRSGPNCIGRFLAV

- continuation -

for SEQ ID NO: 651

Wed Jun 4 11:54:11 2003

us-09-873-3

Db 961 |||||||GAACGGCCACTCACCCCTGATGTCCAGCAGAAAGTCAGAAGGAATTGATACAGTTA 1020
Qy 1021 CCCAATAAGGCACCACCCACCTATGATACTGTGCTACAGTTGGAGTATCTTGACATGGTG 1080
Db 1021 CCCAATAAGGCACCACCCACCTATGATACTGTGCTACAGTTGGAGTATCTTGACATGGTG 1080
Qy 1081 GTGAATGAAACACTCAGATTATCCTGCTATGAGACTTGAGAGGGCTGCAAAAAA 1140
Db 1081 GTGAATGAAACACTCAGATTATCCTGCTATGAGACTTGAGAGGGCTGCAAAAAA 1140
Qy 1141 GATGTTGAAATCAATGGATGTTATCCCAAAGGGTGGTGGTGAATGATTCCAAGCTAT 1200
Db 1141 GATGTTGAAATCAATGGATGTTATCCCAAAGGGTGGTGGTGAATGATTCCAAGCTAT 1200
Qy 1201 GTTCTTCATGACCCAAAGTACTGGACAGAGCCTGAGAAGTTCCCTCCCTGAAAGGTC 1260
Db 1201 GTTCTTCATGACCCAAAGTACTGGACAGAGCCTGAGAAGTTCCCTCCCTGAAAGGTC 1260
Qy 1261 AGTAAAAAGAACAGAACATAGATCCTTACATATACACACCCCTTGGAAAGTGGACCC 1320
Db 1261 AGTAAAAAGAACAGAACATAGATCCTTACATATACACACCCCTTGGAAAGTGGACCC 1320
Qy 1321 AGAAACTGCATTGGCATGAGGTTGCTCTCGTAACATGAAACTTGCTCTAGTCAGAGTC 1380
Db 1321 AGAAACTGCATTGGCATGAGGTTGCTCTCGTAACATGAAACTTGCTCTAGTCAGAGTC 1380
Qy 1381 CTTCAAGAATTCTCTCTCAAACCTTGAAAGAAACACAGATCCCCCTGAAATTACGCTT 1440
Db 1381 CTTCAAGAATTCTCTCTCAAACCTTGAAAGAAACACAGATCCCCCTGAAATTACGCTT 1440
Qy 1441 GGAGGACTTCTCTAAACAGAAAAACCCATTGTTCTAAAGGCTGAGTCAGGGATGAGACC 1500
Db 1441 GGAGGACTTCTCTAAACAGAAAAACCCATTGTTCTAAAGGCTGAGTCAGGGATGAGACC 1500
Qy 1501 GTAAAGTGGAGCCTGATTTCCCTAAGGACTTCTGGTTGCTTTAAGAAAGCTGTGCCCC 1560
Db 1501 GTAAAGTGGAGCCTGATTTCCCTAAGGACTTCTGGTTGCTTTAAGAAAGCTGTGCCCC 1560
Qy 1561 AGAACACCCAGAGACCTCAAATTACTTTACAATAGAACCCCTGAAATGAAGACGGGCTCA 1620
Db 1561 AGAACACCCAGAGACCTCAAATTACTTTACAATAGAACCCCTGAAATGAAGACGGGCTCA 1620
Qy 1621 TCCAAATGTGCTGCATAAAATAATCAGGGATTCTGTACGTGCAATTGTGCTCTCATGGCT 1680
Db 1621 TCCAAATGTGCTGCATAAAATAATCAGGGATTCTGTACGTGCAATTGTGCTCTCATGGCT 1680
Qy 1681 GTATAGAGTGTATACTGGTAATATAGAGGAGATGACCAATCACTGCTGGGAAGTAG 1740
Db 1681 GTATAGAGTGTATACTGGTAATATAGAGGAGATGACCAATCACTGCTGGGAAGTAG 1740
Qy 1741 ATTTGGCTCTGCTCTCATAGGACTATCTCCACCCACCCAGTAGCACCAATTAACT 1800
Db 1741 ATTTGGCTCTGCTCTCATAGGACTATCTCCACCCACCCAGTAGCACCAATTAACT 1800
Qy 1801 CCTCCTGAGCTCTGATAACATAATTAAACATTCTCAATAATTCAACCAACATTAAT 1860
Db 1801 CCTCCTGAGCTCTGATAACATAATTAAACATTCTCAATAATTCAACCAACATTAAT 1860
Qy 1861 AAAAATAGGAATTATTTGATGGCTCTAACAGTGCACATTATATCATGTGTTATCTGT 1920
Db 1861 AAAAATAGGAATTATTTGATGGCTCTAACAGTGCACATTATATCATGTGTTATCTGT 1920
Qy 1921 AGTATTCTATAGTAACCTTATATTAAAGCAATCAATAAAACCTTAC 1971
Db 1921 AGTATTCTATAGTAACCTTATATTAAAGCAATCAATAAAACCTTAC 1971

RESULT 2
 AW967166/C
 LOCUS AW967166 659 bp mRNA linear EST 01-JUN-2000
 DEFINITION EST379240 MAGE resequences, MAGJ Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW967166
 VERSION AW967166.1 GI:8157002
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

SEQ ID NO: 865

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS 1 (bases 1 to 659)
 Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
 ,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
 Quackenbush,J.
 TITLE Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element cDNA microarray
 JOURNAL Unpublished (2000)
 COMMENT Contact: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@tigr.org
 Plate: 237
 FEATURES Seq primer: Reverse.
 source Location/Qualifiers
 1. .659
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="MAGE resequences, MAGJ"
 /note="Vector: pBluescriptSK"
 BASE COUNT 213 a 125 c 148 g 173 t
 ORIGIN

Query Match 92.3%; Score 389.6; DB 10; Length 659;
 Best Local Similarity 95.3%; Pred. No. 3.4e-72;
 Matches 403; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

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  Qy 1 TGTGTTTTTNTGATTCTCATGTACTTCATTATTATTAAATNANCNAANCCGT 60
  Db 455 TTTTTTCTTGGTATTCTCATGTACTTCATTATTAAATAAGCAAAGCCGT 396
  Qy 61 AAGGGANTNCCTTGCTAGTCNTCCGACTNTGNTNATCTCATCTGACTAATCNGAA 120
  Db 395 AAGGGGAGCCTTGCTAGTCCTCGACTCTGATTCATCTCATCTGACTAATCNGAA 336
  Qy 121 GTAACNAAG-TCGTAGGTCTCCTGTAGATGCAANCANTCGAAGCCAATCAGGAAGATT 179
  Db 335 GTAACGAAGTTCGTAGGTCTCCTGTAGATGCAACCACACTCGAAGCCAATCAGGAAGATT 276
  Qy 180 GTTCTCTTAAGGTATTCTTGGTAAGGTATTCAAATACCTTTAGAGAACTGTTCTC 239
  Db 275 GTTCTCTTAAGGTATTCTTGGTAAGGTATTCAAATACCTTTAGAGAACTGTTCTC 216
  Qy 240 AGAAACAACGTGATTATTCTTGGTAAGGTATTCAAATACCTTTAGAGAACTGTTCTC 299
  Db 215 AGAAACAACGTGATTATTCTTGGTAAGGTATTCAAATACCTTTAGAGAACTGTTCTC 156
  Qy 300 AGTTTGCCATTGACTTTAACCTTCTCCGTAGAAATTGCTAAAATTCCAGAACATCAA 359
  Db 155 AGTTTGCCATTGACTTTAACCTTCTCCGTAGAAATTGCTAAAATTCCAGAACATCAA 96
  Qy 360 AATTCCATCTTCTACTGGATGAGTAAGGTCAAATTAAACCTCCAGGTTGACCTTGGG 419
  Db 95 AATTCCATCTTCTACTGGATGAGTAAGGTCAAATTAAACCTCCAGGTTGACCTTGGG 36
  Qy 420 CTT 422
  Db 35 CTT 33
  
```

ALIGNMENTS

SEQ ID NO: 1015

RESULT 1
 N22479
 LOCUS N22479 354 bp mRNA linear EST 20-DEC-1995
 DEFINITION yw35all.s1 Morton Fetal Cochlea Homo sapiens cDNA clone
 IMAGE:254204 3', mRNA sequence.
 ACCESSION N22479
 VERSION N22479.1 GI:1128613
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 354)
 AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
 Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
 ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
 ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
 Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
 Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
 TITLE Generation and analysis of 280,000 human expressed sequence tags
 JOURNAL Genome Res. 6 (9), 807-828 (1996)
 MEDLINE 97044478
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 268

Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 484 Std Error: 0.00
 Seq primer: m13 -40 forward
 High quality sequence stop: 268.

FEATURES Location/Qualifiers
 source 1..354
 /organism="Homo sapiens"
 /db_xref="GDB:3891657"
 /db_xref="taxon:9606"
 /clone="IMAGE:254204"
 /clone_lib="Morton Fetal Cochlea"
 /tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /note="Organ: ear; Vector: pBluescript SK-; Site_1: EcoRI;
 Site_2: XbaI; Reference: Genomics 23, 42-50 (1994) Cloned
 unidirectionally. Primer: Oligo dT. Fetal cochlea, normal.
 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
 XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAATTCGGCAGG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"

BASE COUNT 120 a 68 c 37 g 129 t
 ORIGIN

Query Match 100.0%; Score 354; DB 14; Length 354;
 Best Local Similarity 100.0%; Pred. No. 1.3e-46;
 Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TTTTTTTTTTTTTTGTCAATCCATAAAGTTATTTAAAAACTGTTAAAAACTAA	60
Db	1	TTTTTTTTTTTTTTGTCAATCCATAAAGTTATTTAAAAACTGTTAAAAACTAA	60
Qy	61	CCATACAGGTTTATTATATACTTAAAAAGTTGTCCTATGTTGAAGTAAATACATT	120
Db	61	CCATACAGGTTTATTATATACTTAAAAAGTTGTCCTATGTTGAAGTAAATACATT	120
Qy	121	AGCAACATCTCCGGACACCCTTTATAAAAGTAAACTCTAGATCCTGAAATGTACT	180
Db	121	AGCAACATCTCCGGACACCCTTTATAAAAGTAAACTCTAGATCCTGAAATGTACT	180
Qy	181	ACAGTAGAGTCTATAGTTACACTTTAATCACAGATGGAATTCATCTCCTTACTCCC	240
Db	181	ACAGTAGAGTCTATAGTTACACTTTAATCACAGATGGAATTCATCTCCTTACTCCC	240
Qy	241	CTACTTCCCACATGTGGCAGTTATTACTTCAAAATTAAATGACATTCACTCATGTTACT	300
Db	241	CTACTTCCCACATGTGGCAGTTATTACTTCAAAATTAAATGACATTCACTCATGTTACT	300
Qy	301	ACCACAGATCCTAAATAGAGTACATACTGCATAATTACTAACAGAGCCAGTCT	354
Db	301	ACCACAGATCCTAAATAGAGTACATACTGCATAATTACTAACAGAGCCAGTCT	354

RESULT 4
 AA251562/c
 ID AA251562 standard; cDNA; 580 BP.
 XX
 AC AA251562;
 XX
 DT 21-JUN-2000 (first entry)
 XX
 DE Human hypoxia response regulating gene, 77H4 related cDNA clone 18E.
 XX
 KW Hypoxia response regulating gene; gene 77H4; human; EST 18E; cardiant;
 KW apoptosis; angiogenesis; vasotropic; cytostatic; ophthalmological;
 KW cerebroprotective; antagonist; regulator; inhibitor; treatment; tumour;
 KW hypoxia associated pathology; HAP; gene therapy; diagnosis; ischaemia;
 KW steroid receptor coactivator; SRA; retinopathy; myocardial infarction;
 KW stroke; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT polyA_signal 536..541
 FT /*tag- a
 XX
 PN WO200012525-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 27-AUG-1999; 99WO-US20394.
 XX
 PR 27-AUG-1998; 98US-0098158.
 PR 05-MAY-1999; 99US-0132684.
 XX
 PA (QUAR-) QUARK BIOTECH INC.
 PA (KOHN/) KOHN K.
 XX
 PI Einat P, Skaliter R, Feinstein E;
 XX
 DR WPI; 2000-256577/22.
 XX
 PT Novel polynucleotides capable of regulating angiogenesis or apoptosis
 PT useful for diagnosis and treatment of hypoxia, ischemia and tumor
 PT growth.
 XX
 PS Claim 1; Fig 7a; 78pp; English.
 XX
 CC The present sequence is the human hypoxia response regulating gene,
 CC 77H4, related cDNA clone 18E. The gene 77H4 has similarity to steroid
 CC receptor transcriptional co-activator, SRA function and can serve as
 CC a coactivator in some transcriptional complexes. It has vasotropic,
 CC cardiant, ophthalmological, cytostatic and cerebroprotective activity.
 CC Antagonist of the encoded protein, functions as a regulator of apoptosis
 CC or angiogenesis. The protein encoded by this polynucleotide, the
 CC biologically active product from enzymatic activity of the protein or
 CC inhibitor of the enzymatic activity is useful for regulating hypoxia
 CC and associated pathologies (HAP). It is useful for gene therapy, diagnosis
 CC and treatment of tumour growth and ischaemia, e.g., retinopathy,
 CC myocardial infarction and stroke.
 XX
 SQ Sequence 580 BP; 177 A; 111 C; 134 G; 158 T; 0 other;
 Query Match 97.5%; Score 428; DB 21; Length 580;
 Best Local Similarity 99.8%; Pred. No. 1.3e-125;
 Matches 439; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 Qy 1 TTTTGATTTAAAAGATTTATTTCTTATGCAGGTAGGCAGTTAGAAATTCAAAGTC 60
 Db 558 TTTTGATTTAAAAGATTTATTTCTTATGCAGGTAGGCAGTTAGAAATTCAAAGTC 499
 Qy 61 TAACAATGACATTCTGAAAGTGGCACAG-CTTTAAACTCAGGCTATGTATACAGTAAC 119
 Db 498 TAACAATGACATTCTGAAAGTGGCACAGCCTTAAACTCAGGCTATGTATACAGTAAC 439
 Qy 120 CTTGTGAACTGGTCTAGCCAGATCTTCACTTCATGAAAGCACAGGTCTGCTCTTTC 179
 Db 438 CTTGTGAACTGGTCTAGCCAGATCTTCACTTCATGAAAGCACAGGTCTGCTCTTTC 379
 Qy 180 TTTCAGAGGCTCTCATATTCCATCGCCAGTTCTGTTACAAGGCAGACTGAATCA 239
 Db 378 TTTCAGAGGCTCTCATATTCCATCGCCAGTTCTGTTACAAGGCAGACTGAATCA 319
 Qy 240 AGCCAAGATCAACACACACTGGTACACGGCTCCAAACCAATTATATATATAT 299
 Db 318 AGCCAAGATCAACACACACTGGTACACGGCTCCAAACCAATTATATATATAT 259
 Qy 300 ATTCTACTTCCAAACACCCGATTATCCGGTCAATCAAAGCCTGGTTGGCCAAACAA 359
 Db 258 ATTCTACTTCCAAACACCCGATTATCCGGTCAATCAAAGCCTGGTTGGCCAAACAA 199
 Qy 360 TAAACTCGTCAGGAGATCGAAGGTTGAGATGTCAGTGGCTCCCTGGAGGTCCAG 419
 Db 198 TAAACTCGTCAGGAGATCGAAGGTTGAGATGTCAGTGGCTCCCTGGAGGTCCAG 139
 Qy 420 TGGTGAATCCCTCTTCCAAA 439
 Db 138 TGGTGAATCCCTCTTCCAAA 119

SEQ ID NO: 1027

RESULT 1
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 LOCUS N98464 439 bp mRNA linear EST 20-AUG-1996
 DEFINITION zb86b06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
 clone IMAGE:310451 3', mRNA sequence.
 ACCESSION N98464
 VERSION N98464.1 GI:1269909
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 439)
 AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
 Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
 ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
 ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
 Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
 Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
 TITLE Generation and analysis of 280,000 human expressed sequence tags
 JOURNAL Genome Res. 6 (9), 807-828 (1996)
 MEDLINE 97044478
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 568 Std Error: 0.00
 Seq primer: mob.REGA+ET

FEATURES High quality sequence stop: 377.
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 /db_xref="GDB:1253865"
 /db_xref="taxon:9606"
 /clone="IMAGE:310451"
 /clone_lib="Soares_senescent_fibroblasts_NbHSF"
 /tissue_type="senescent fibroblast"
 /lab_host="DH10B (ampicillin resistant)"
 /note="vector: pT7T3D (Pharmacia) with a modified
 polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
 ; 1st strand cDNA was primed with a Not I - oligo(dT)
 primer [5'
 TGTTACCAATCTGAAGTGGGAGCGGCCGATTTTTTTTTTTTTTTT 3',
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo."

BASE COUNT 118 a 101 c 83 g 137 t
 ORIGIN

Query Match 100.0%; Score 439; DB 14; Length 439;
 Best Local Similarity 100.0%; Pred. No. 1.e-110;
 Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TTTTGATTTAAAAGATTTTATTCTTATGCAAGTAGGCAGTTAGAAATTCAAAGTC 60
 Db 1 TTTTGATTTAAAAGATTTTATTCTTATGCAAGTAGGCAGTTAGAAATTCAAAGTC 60
 Qy 61 TAACAATGACATTCTTGAAGTGGGCACAGCTTTAAACTCAGGCTATGTATACAGTAACC 120
 Db 61 TAACAATGACATTCTTGAAGTGGGCACAGCTTTAAACTCAGGCTATGTATACAGTAACC 120
 Qy 121 TTGTGGAACTGGTCAGCCAGATCTTCACTTCATGAAAGCACAGGGTCTGCTCTTCT 180
 Db 121 TTGTGGAACTGGTCAGCCAGATCTTCACTTCATGAAAGCACAGGGTCTGCTCTTCT 180
 Qy 181 TTCCAGAGGGCTCTCATATTCCATGCCAGTTCTGTACAAGGCAGACTGAATCAA 240
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 Db 241 GCCAAGATCAACACACACTGGTACACCGTGGCTCCAACCAATTATATGTATATATA 300
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 Db 301 TTCTACTTCAACACCCGCATTCATCTGGTCAATCAAAGCCTGGTTGGCCAACAAAT 360
 Qy 361 AAACTCGTCAAGGAGATCGAAGGTTGTAGATGTCAGTCACGTGGCTTGGAGGTCCAGT 420
 Db 361 AAACTCGTCAAGGAGATCGAAGGTTGTAGATGTCAGTCACGTGGCTTGGAGGTCCAGT 420
 Qy 421 GGTGACTCCCTTCCAAA 439
 Db 421 GGTGACTCCCTTCCAAA 439

RESULT 1
W90146
LOCUS W90146 304 bp mRNA linear EST 07-MAY-1997
DEFINITION zh75e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
ACCESSION W90146 clone IMAGE:417916 3', mRNA sequence.
VERSION W90146.1 GI:1406136
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 ('bases 1 to 304)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free, through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1214 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 267.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="GDB:1326386"
/db_xref="taxon:9606"
/clone="IMAGE:417916"
/clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen 1NFLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer. [5'
AACTGGAAGAATTAAATTAAAGATCTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 86 a 72 c 45 g 100 t 1 others
ORIGIN

Query Match 99.7%; Score 303; DB 14; Length 304;
Best Local Similarity 100.0%; Pred. No. 5e-75;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CACTTATGCCAATTTAATAATCCATATTAACGTGATGTGAAAAATGTCTTATGA 60
Db 1 CACTTATGCCAATTTAATAATCCATATTAACGTGATGTGAAAAATGTCTTATGA 60
Qy 61 TCTGTTACCAACCCAAAAGAATGCATCATAACTTCAGANTATGTTCTTGACTTCAAC 120
Db 61 TCTGTTACCAACCCAAAAGAATGCATCATAACTTCAGANTATGTTCTTGACTTCAAC 120
Qy 121 CTCTGCTCTTCTTACAATTACCTTGGCTGGCCAGACATGCTCCTGTTAATGACTC 180
Db 121 CTCTGCTCTTCTTACAATTACCTTGGCTGGCCAGACATGCTCCTGTTAATGACTC 180
Qy 181 TACATTTACTCGCACAGCGTTGTCTGGACTCTCTGCTAATCGATGAACAAACAGTA 240
Db 181 TACATTTACTCGCACAGCGTTGTCTGGACTCTCTGCTAATCGATGAACAAACAGTA 240
Qy 241 AACAGTTCAGATGGACCAATAAGTCACCACTTTCTCCAGACCGAAGTTGGAGGGCTCT 300
Db 241 AACAGTTCAGATGGACCAATAAGTCACCACTTTCTCCAGACCGAAGTTGGAGGGCTCT 300
Qy 301 TTCC 304
Db 301 TTCC 304